

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
20 October 2005 (20.10.2005)

PCT

(10) International Publication Number
WO 2005/097822 A1

(51) International Patent Classification⁷: **C07K 14/155**,
A61P 31/18, G01N 33/569, A61K 39/21, 38/16, C07K
7/08

R3T 5V4 (CA). **PLUMMER, Francis, A.**, [CA/CA]; 631
Drake Centre, Winnipeg, Manitoba R3T 5V4R (CA).

(21) International Application Number:
PCT/CA2005/000547

(74) Agent: **ADE & COMPANY**; 1700-360 Main Street, Win-
nipeg, Manitoba R3C 3Z3 (CA).

(22) International Filing Date: 11 April 2005 (11.04.2005)

(81) Designated States (unless otherwise indicated, for every
kind of national protection available): AE, AG, AL, AM,
AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE,
KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM,
PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY,
TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU,
ZA, ZM, ZW.

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/560,601 9 April 2004 (09.04.2004) US

(71) Applicant (for all designated States except US): **UNIVER-
SITY OF MANITOBA** [CA/CA]; Industry Liaison Office,
631 Drake Centre, Winnipeg, Manitoba R3T 5V4 (CA).

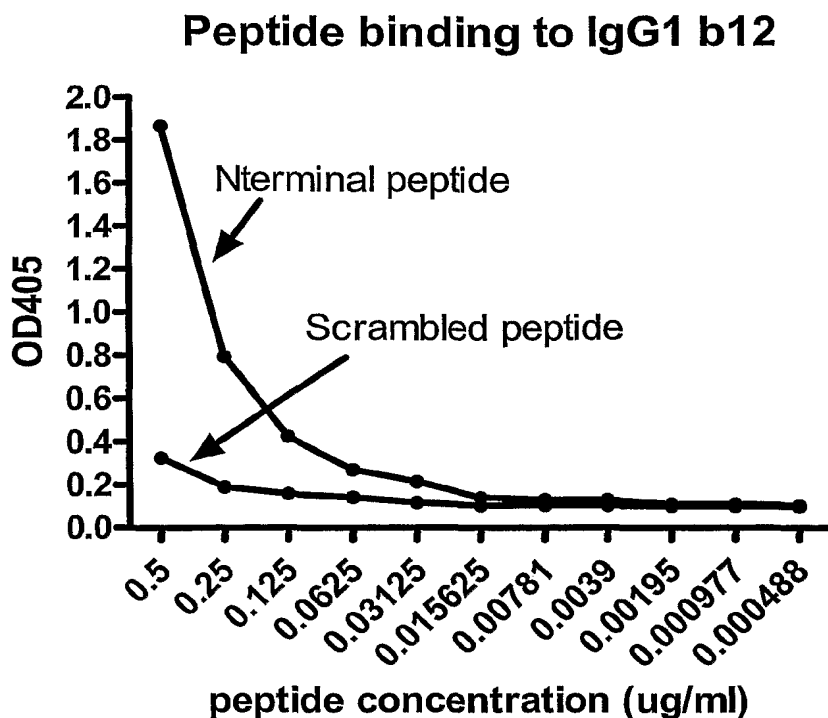
(84) Designated States (unless otherwise indicated, for every
kind of regional protection available): ARIPO (BW, GH,
GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM,
ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI,
FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO,
SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN,
GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **WARUK, Jillian
L.M.**, [CA/CA]; 631 Drake Centre, Winnipeg, Manitoba
R3T 5V4 (CA). **BERRY, Jody, D.**, [CA/CA]; 631 Drake
Centre, Winnipeg, Manitoba R3T 5V4 (CA). **BALL, T.
Blake**, [CA/CA]; 631 Drake Centre, Winnipeg, Manitoba

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(54) Title: IDENTIFICATION OF THE PRECISE AMINO ACID SEQUENCE OF THE EPITOPE RECOGNIZED BY THE PO-
TENT NEUTRALIZING HUMAN ANTI-HIV-1 MONOCLONAL ANTIBODY IGG1B12



(57) Abstract: The IgG1b12 human monoclonal antibody binds gp120 strongly, and is the most potent HIV neutralizing antibody known. The exact amino acid sequence of this binding site is not known. We identified the minimal parts of the HIV-1 gp120 (envelope) protein, which IgG1b12 binds to. We did this by quadrupole time of flight (QqTOF) mass spectrometry using epitope excision. Epitope excision allows for determination of conformational epitopes. To do this we bound gp120 to IgG1b12, digested off all unbound portions of gp120, and then ran mass spectrometry of the resulting IgG1b12-gp120 peptide complex. The results allow us to determine the exact amino acid sequence involved in IgG1b12-gp120 interaction.

WO 2005/097822 A1

**Published:**

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

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